REMARKS

As described below, this application is in condition for immediate allowance. The above amendments and the following descriptions confirm that all of the asserted rejections are now in conditions for withdrawal.

Claims 33 and 47 have been amended. Claims 28, 29, 32-34(a)-(d), 35 and 47 remain in the application. New claims 48-49 have been added. Reexamination and allowance of the amended claims are requested.

The Examiner has objected to the specification and Figures because they contain sequences that are not identified by SEQ ID NO. The addition of SEQ ID NOs to the present specification and Figures are being sent under separate cover.

The Examiner has rejected claims 28, 29, 32, 33, 34(a)-(d), 35 and 47 under 35 U.S.C. § 112, first paragraph, for purported lack of written description and for purported lack of enablement for "at least part of the PLAG1 gene" and "degenerate sequences thereof." In response, claims 33 and 47 have been amended, in respect to PLAG 1, to remove the references to degenerate sequences, and to refer to the complementary sequence or the antisense version of the nucleic acid. Support for these amendments is found on page 10, lines 26 and 29 of the specification. Support for antisense sequences is also provided in Example 12 of the specification.

The proteins of the invention are characterized by the presence of a specific zinc finger sequence, and no sequence similarity is apparent to any known zinc finger protein in the prior art (see page 41, lines 10-11 of the specification). Enablement is provided in Example 2, point 3.2, in which methods are disclosed for finding sequences with unknown function and assembling these sequences into aligned nucleic acids with sequence similarities to about 75% at the amino acid level in the region of the new PLAG1 gene encoding zinc fingers 4 to 7 (see page 41, lines 12-22 of the specification). Furthermore, these anonymous

sequences have been mapped to a chromosomal region which, like the PLAG1 gene, is implicated in tumors of the salivary glands (see page 41, lines 23-25 of the specification). Accordingly, the nucleic acids of the invention have been redefined in amended claims 33 and 47. Furthermore, another working example demonstrating how to identify PLAG-1 related genes is disclosed in Example 3 and resulted in the isolation of PLAG2 cDNA. Because the written description demonstrates the production of at least two similar sequences comprising the zinc finger motifs of the present invention, it is believed that the claims are enabled by the specification and what is known to the person skilled in the art.

The Examiner has rejected claims 33 and 47 under 35 U.S.C. § 102(b) for purported anticipation by Kraus et al. (Genomics, 23, pages 272-274, December 1994). The Examiner asserts that Kraus discloses an isolated nucleotide sequence wherein the nucleic acid is an oligonucleotide and a polynucleotide fragment having a sequence of at least a part of a gene of the PLAG1 subfamily. The Examiner also asserts that Kraus discloses a nucleic acid having a nucleotide sequence of at least a part of a T-gene selected from the group consisting of the PLAG1 subfamily of zinc finger protein genes, the CTNNB1 gene and fusion protein, or complementary degenerate versions of the nucleotide sequence. In response, claims 33 and 47 have been amended, in respect to PLAG 1, to remove the references to degenerate sequences, and to refer to the complementary sequence or the antisense version of the nucleic acid. Claim 33 has been amended to remove the reference to uncombined CTNNB1, and now refers to CTNNB1 only in the context of fusions between the PLAG1 gene and CTNNB1 gene. The fusions between the PLAG1 gene and the CTNNB1 described in the amended claim 33 are novel, as identified by the t(3,8)(p21;q12) translocation. Several examples of fusions identified in the present invention are described and methods for their production are disclosed in Example 2 and Figure 6. These fusions

have not been described by Kraus. Therefore, it is believed that the substances of Kraus do not anticipate the substances of the present invention.

The Examiner has rejected claims 47, 32, 33, 34 (a)–(d), and 35 under 35 U.S.C. § 102(a) for purported anticipation by Nollet et al. (*Genomics*, March 1996). The Examiner asserts that Nollet et al. discloses a nucleic acid in isolated form wherein the nucleic acid is an oligonucleotide and a polynucleotide fragment having a sequence having at least a part of a gene in the PLAG1 gene subfamily. Claim 33 has been amended to refer to fusions between the PLAG1 gene and the CTBBB1 gene as identified by the t(3,8)(p21;q12) translocation. These fusions have not been described by Nollet. Claim 47 has been amended to exclude polypeptides with less than 75% sequence identity to a polypeptide sequence of PLAG1 in the region from zinc fingers 4 to 7. Support for this level of sequence identity is found on page 41, line 21 of the specification. The claimed level of sequence identity distinguishes the present invention from the description provided by Nollet. Therefore, it is believed that the nucleic acid of Nollet et al. does not anticipate the nucleic acid of the present invention.

In view of the above amendments and remarks, it is believed that the claims are in condition for allowance. Reconsideration of the rejections is requested. Allowance of claims 28, 29, 32-34 (a)-(d), 35 and 47-49 is respectfully requested.

Respectfully submitted,

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MARKED-UP AMENDED CLAIMS

33. (Twice amended) A macromolecule comprising a [derivative of a] nucleic acid in isolated form, comprising [one] a fusion of at least two of an oligonucleotide, a polynucleotide and a gene having a nucleotide sequence of at least part of a T-gene selected from the group consisting of the *PLAG* (pleomorphic adenoma gene 1) subfamily of zinc finger protein genes, and at least part of the *CTNNB1* (β catenin) gene and fusions thereof, or complementary or [degenerate] antisense versions of the nucleotide sequence.

47. (Twice amended) A nucleic acid in isolated form wherein the nucleic acid is one of an oligonucleotide, a polynucleotide and a gene having a sequence of at least part of the PLAG1 (pleomorphic adenoma gene 1) gene, [sequences] or the complementary [thereto and degenerate sequences thereof] sequence or antisense version of the nucleic acid; wherein a protein encoded by the nucleic acid comprises a polypeptide sequence which is at least 75% identical to a polypeptide sequence of PLAG 1 in the region from zinc fingers 4 to 7.